



SEQUENCE LISTING

<110> Acton, Susan L. *et al.*<120> ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
DIAGNOSTIC USES THEREFOR

<130> MNI-132CP

<140> 09/163,648

<141> 1998-09-30

<150> 08/989,299

<151> 1997-12-11

<160> 24

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<213> Homo sapiens

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<212> PRT

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Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu
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 Leu Lys Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp
 340 345 350
 Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn
 355 360 365
 Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His
 370 375 380
 Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln
 385 390 395 400
 Cys Thr Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met
 405 410 415
 Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu
 420 425 430
 Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu
 435 440 445
 Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu
 450 455 460

Ser Ser Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met Lys
 465 470 475 480
 Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val Asp
 485 490 495
 Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr
 500 505 510
 Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro
 515 520 525
 Pro Val Pro Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe His
 530 535 540
 Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile Ile
 545 550 555 560
 Gln Phe Gln Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr Gly
 565 570 575
 Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln Arg
 580 585 590
 Leu Ala Thr Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu Ala
 595 600 605
 Met Gln Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Leu
 610 615 620
 Ser Tyr Phe Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu Leu
 625 630 635 640
 His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn Ser
 645 650 655
 Ala Arg Ser Glu Gly Pro Leu Pro Asp Ser Gly Arg Val Ser Phe Leu
 660 665 670
 Gly Leu Asp Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp Leu Leu
 675 680 685
 Leu Phe Leu Gly Ile Ala Leu Leu Val Ala Thr Leu Gly Leu Ser Gln
 690 695 700
 Arg Leu Phe Ser Ile Arg His Arg Ser Leu His Arg His Ser His Gly
 705 710 715 720
 Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser
 725 730

<210> 5

<211> 732

<212> PRT

<213> Murine sp.

<220>

<223> Description of Artificial Sequence: motifs

<400> 5

Met	Gly	Gln	Gly	Trp	Ala	Thr	Pro	Gly	Leu	Pro	Ser	Phe	Leu	Phe	Leu			
1				5					10					15				
Leu	Leu	Cys	Cys	Gly	His	His	Leu	Leu	Val	Leu	Ser	Gln	Val	Ala	Thr			
			20					25					30					
Asp	His	Val	Thr	Ala	Asn	Gln	Gly	Ile	Thr	Asn	Gln	Ala	Thr	Thr	Arg			
		35					40					45						
Ser	Gln	Thr	Thr	Thr	His	Gln	Ala	Thr	Ile	Asp	Gln	Thr	Thr	Gln	Ile			
	50					55					60							
Pro	Asn	Leu	Glu	Thr	Asp	Glu	Ala	Lys	Ala	Asp	Arg	Phe	Val	Glu	Glu			
	65				70					75				80				
Tyr	Asp	Arg	Thr	Ala	Gln	Val	Leu	Leu	Asn	Glu	Tyr	Ala	Glu	Ala	Asn			
				85					90					95				
Trp	Gln	Tyr	Asn	Thr	Asn	Ile	Thr	Ile	Glu	Gly	Ser	Lys	Ile	Leu	Leu			
			100					105					110					
Glu	Lys	Ser	Thr	Glu	Val	Ser	Asn	His	Thr	Leu	Lys	Tyr	Gly	Thr	Arg			
		115					120					125						
Ala	Lys	Thr	Phe	Asp	Val	Ser	Asn	Phe	Gln	Asn	Ser	Ser	Ile	Lys	Arg			
	130					135					140							
Ile	Ile	Lys	Lys	Leu	Gln	Asn	Leu	Asp	Arg	Ala	Val	Leu	Pro	Pro	Lys			
	145				150					155					160			
Glu	Leu	Glu	Glu	Tyr	Asn	Gln	Ile	Leu	Leu	Asp	Met	Glu	Thr	Thr	Tyr			
				165				170						175				
Ser	Leu	Ser	Asn	Ile	Cys	Tyr	Thr	Asn	Gly	Thr	Cys	Met	Pro	Leu	Glu			
			180					185					190					
Pro	Asp	Leu	Thr	Asn	Met	Met	Ala	Thr	Ser	Arg	Lys	Tyr	Glu	Glu	Leu			
		195					200					205						
Leu	Trp	Ala	Trp	Lys	Ser	Trp	Arg	Asp	Lys	Val	Gly	Arg	Ala	Ile	Leu			
	210					215					220							
Pro	Phe	Phe	Pro	Lys	Tyr	Val	Glu	Phe	Ser	Asn	Lys	Ile	Ala	Lys	Leu			
	225				230					235					240			
Asn	Gly	Tyr	Thr	Asp	Ala	Gly	Asp	Ser	Trp	Arg	Ser	Leu	Tyr	Glu	Ser			
				245					250					255				
Asp	Asn	Leu	Glu	Gln	Asp	Leu	Glu	Lys	Leu	Tyr	Gln	Glu	Leu	Gln	Pro			
			260					265					270					
Leu	Tyr	Leu	Asn	Leu	His	Ala	Tyr	Val	Arg	Arg	Ser	Leu	His	Arg	His			
		275					280					285						
Tyr	Gly	Ser	Glu	Tyr	Ile	Asn	Leu	Asp	Gly	Pro	Ile	Pro	Ala	His	Leu			
	290					295					300							
Leu	Gly	Asn	Met	Trp	Ala	Gln	Thr	Trp	Ser	Asn	Ile	Tyr	Asp	Leu	Val			
	305				310					315				320				

Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr Glu Ala Met Ile
 325 330 335
 Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu Ala Asp Asn Phe
 340 345 350
 Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys
 355 360 365
 Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Pro
 370 375 380
 Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys
 385 390 395 400
 Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His His Glu Met Gly
 405 410 415
 His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Thr Phe Arg
 420 425 430
 Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Ile Met Ala
 435 440 445
 Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu Asn Leu Leu Ser
 450 455 460
 Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe Leu Met Lys Met
 465 470 475 480
 Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Ile Asp Gln
 485 490 495
 Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn
 500 505 510
 Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro
 515 520 525
 Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser Lys Phe His Val
 530 535 540
 Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser Phe Ile Ile Gln
 545 550 555 560
 Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly His Thr Gly Pro
 565 570 575
 Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Lys Leu Leu
 580 585 590
 Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp Pro Glu Ala Met
 595 600 605
 Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Met Asn
 610 615 620
 Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu Asn Arg Arg His
 625 630 635 640

Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala Pro Asn Thr Ala
 645 650 655
 Arg Ala Glu Gly Ser Thr Ala Glu Ser Asn Arg Val Asn Phe Leu Gly
 660 665 670
 Leu Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly Gln Trp Val Leu Leu
 675 680 685
 Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val Gly Leu Ala His Arg
 690 695 700
 Leu Tyr Asn Ile Arg Asn His His Ser Leu Arg Arg Pro His Arg Gly
 705 710 715 720
 Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser
 725 730

<210> 6

<211> 737

<212> PRT

<213> *Oryctolagus cuniculus*

<220>

<223> Description of Artificial Sequence: motifs

<400> 6

Met Gly Gln Gly Trp Ala Ala Pro Gly Leu Pro Ser Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Cys Cys Gly His Ser Leu Leu Val Pro Ser Arg Val Ala Ala
 20 25 30
 Arg Arg Val Thr Val Asn Gln Gly Thr Thr Ser Gln Ala Thr Thr Thr
 35 40 45
 Ser Lys Ala Thr Thr Ser Ile Arg Ala Thr Thr His Gln Thr Thr Ala
 50 55 60
 His Gln Thr Thr Gln Ser Pro Asn Leu Val Thr Asp Glu Ala Glu Ala
 65 70 75 80
 Ser Arg Phe Val Glu Glu Tyr Asp Arg Ser Phe Gln Ala Val Trp Asn
 85 90 95
 Glu Tyr Ala Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu
 100 105 110
 Ala Ser Lys Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr
 115 120 125
 Leu Thr Tyr Gly Asn Trp Ala Arg Arg Phe Asp Val Ser Asn Phe Gln
 130 135 140
 Asn Ala Thr Ser Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Gln Arg
 145 150 155 160
 Ala Val Leu Pro Val Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu
 165 170 175

Asp Met Glu Thr Ile Tyr Ser Val Ala Asn Val Cys Arg Val Asp Gly
 180 185 190
 Ser Cys Leu Gln Leu Glu Pro Asp Leu Thr Asn Leu Met Ala Thr Ser
 195 200 205
 Arg Lys Tyr Asp Glu Leu Leu Trp Val Trp Thr Ser Trp Arg Asp Lys
 210 215 220
 Val Gly Arg Ala Ile Leu Pro Tyr Phe Pro Lys Tyr Val Glu Phe Thr
 225 230 235 240
 Asn Lys Ala Ala Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp
 245 250 255
 Arg Ser Met Tyr Glu Thr Pro Thr Leu Glu Gln Asp Leu Glu Arg Leu
 260 265 270
 Phe Gln Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Gly
 275 280 285
 Arg Ala Leu His Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly
 290 295 300
 Pro Ile Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser
 305 310 315 320
 Asn Ile Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Ser Thr Met Asp
 325 330 335
 Ala Thr Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Met Phe
 340 345 350
 Glu Glu Ala Asp Lys Phe Phe Ile Ser Leu Gly Leu Leu Pro Val Pro
 355 360 365
 Pro Glu Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg
 370 375 380
 Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp
 385 390 395 400
 Phe Arg Ile Lys Gln Cys Thr Thr Val Asn Met Glu Asp Leu Val Val
 405 410 415
 Val His His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp
 420 425 430
 Leu Pro Val Ala Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala
 435 440 445
 Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His
 450 455 460
 Ser Ile Asn Leu Leu Ser Ser Glu Gly Gly Gly Tyr Glu His Asp Ile
 465 470 475 480
 Asn Phe Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe
 485 490 495

Ser Tyr Leu Val Asp Glu Trp Arg Trp Arg Val Phe Asp Gly Ser Ile
 500 505 510
 Thr Lys Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr
 515 520 525
 Gln Gly Leu Cys Pro Pro Ala Pro Arg Ser Gln Gly Asp Phe Asp Pro
 530 535 540
 Gly Ala Lys Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe
 545 550 555 560
 Val Ser Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Lys Ala
 565 570 575
 Ala Gly His Thr Gly Pro Leu His Thr Cys Asp Ile Tyr Gln Ser Lys
 580 585 590
 Glu Ala Gly Lys Arg Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys
 595 600 605
 Pro Trp Pro Glu Ala Met Lys Val Ile Thr Gly Gln Pro Asn Met Ser
 610 615 620
 Ala Ser Ala Met Met Asn Tyr Phe Lys Pro Leu Met Asp Trp Leu Leu
 625 630 635 640
 Thr Glu Asn Gly Arg His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Thr
 645 650 655
 Trp Thr Pro Asn Ser Ala Arg Ser Glu Gly Ser Leu Pro Asp Ser Gly
 660 665 670
 Arg Val Asn Phe Leu Gly Met Asn Leu Asp Ala Gln Gln Ala Arg Val
 675 680 685
 Gly Gln Trp Val Leu Leu Phe Leu Gly Val Ala Leu Leu Leu Ala Ser
 690 695 700
 Leu Gly Leu Thr Gln Arg Leu Phe Ser Ile Arg Tyr Gln Ser Leu Arg
 705 710 715 720
 Gln Pro His His Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His
 725 730 735

Ser

<210> 7

<211> 1306

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: motifs

<400> 7

Met Gly Ala Ala Ser Gly Arg Arg Gly Pro Gly Leu Leu Leu Pro Leu
 1 5 10 15

Pro Leu Leu Leu Leu Leu Pro Pro Gln Pro Ala Leu Ala Leu Asp Pro
 20 25 30
 Gly Leu Gln Pro Gly Asn Phe Ser Ala Asp Glu Ala Gly Ala Gln Leu
 35 40 45
 Phe Ala Gln Ser Tyr Asn Ser Ser Ala Glu Gln Val Leu Phe Gln Ser
 50 55 60
 Val Ala Ala Ser Trp Ala His Asp Thr Asn Ile Thr Ala Glu Asn Ala
 65 70 75 80
 Arg Arg Gln Glu Glu Ala Ala Leu Leu Ser Gln Glu Phe Ala Glu Ala
 85 90 95
 Trp Gly Gln Lys Ala Lys Glu Leu Tyr Glu Pro Ile Trp Gln Asn Phe
 100 105 110
 Thr Asp Pro Gln Leu Arg Arg Ile Ile Gly Ala Val Arg Thr Leu Gly
 115 120 125
 Ser Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln Tyr Asn Ala Leu Leu
 130 135 140
 Ser Asn Met Ser Arg Ile Tyr Ser Thr Ala Lys Val Cys Leu Pro Asn
 145 150 155 160
 Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Asp Leu Thr Asn Ile Leu
 165 170 175
 Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe Ala Trp Glu Gly Trp
 180 185 190
 His Asn Ala Ala Gly Ile Pro Leu Lys Pro Leu Tyr Glu Asp Phe Thr
 195 200 205
 Ala Leu Ser Asn Glu Ala Tyr Lys Gln Asp Gly Phe Thr Asp Thr Gly
 210 215 220
 Ala Tyr Trp Arg Ser Trp Tyr Asn Ser Pro Thr Phe Glu Asp Asp Leu
 225 230 235 240
 Glu His Leu Tyr Gln Gln Leu Glu Pro Leu Tyr Leu Asn Leu His Ala
 245 250 255
 Phe Val Arg Arg Ala Leu His Arg Arg Tyr Gly Asp Arg Tyr Ile Asn
 260 265 270
 Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly Asp Met Trp Ala Gln
 275 280 285
 Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro Phe Pro Asp Lys Pro
 290 295 300
 Asn Leu Asp Val Thr Ser Thr Met Leu Gln Gln Gly Trp Asn Ala Thr
 305 310 315 320
 His Met Phe Arg Val Ala Glu Glu Phe Phe Thr Ser Leu Glu Leu Ser
 325 330 335

Pro Met Pro Pro Glu Phe Trp Glu Gly Ser Met Leu Glu Lys Pro Ala
 340 345 350
 Asp Gly Arg Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn
 355 360 365
 Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg Val Thr Met Asp Gln
 370 375 380
 Leu Ser Thr Val His His Glu Met Gly His Ile Gln Tyr Tyr Leu Gln
 385 390 395 400
 Tyr Lys Asp Leu Pro Val Ser Leu Arg Arg Gly Ala Asn Pro Gly Phe
 405 410 415
 His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Glu
 420 425 430
 His Leu His Lys Ile Gly Leu Leu Asp Arg Val Thr Asn Asp Thr Glu
 435 440 445
 Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu Lys Ile Ala Phe
 450 455 460
 Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp Gly Val Phe Ser
 465 470 475 480
 Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp Trp Trp Tyr Leu Arg
 485 490 495
 Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Thr Arg Asn Glu Thr His
 500 505 510
 Phe Asp Ala Gly Ala Lys Phe His Val Pro Asn Val Thr Pro Tyr Ile
 515 520 525
 Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe His Glu Ala Leu
 530 535 540
 Cys Lys Glu Ala Gly Tyr Glu Gly Pro Leu His Gln Cys Asp Ile Tyr
 545 550 555 560
 Arg Ser Thr Lys Ala Gly Ala Lys Leu Arg Lys Val Leu Gln Ala Gly
 565 570 575
 Ser Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met Val Gly Leu Asp
 580 585 590
 Ala Leu Asp Ala Gln Pro Leu Leu Lys Tyr Phe Gln Pro Val Thr Gln
 595 600 605
 Trp Leu Gln Glu Gln Asn Gln Gln Asn Gly Glu Val Leu Gly Trp Pro
 610 615 620
 Glu Tyr Gln Trp His Pro Pro Leu Pro Asp Asn Tyr Pro Glu Gly Ile
 625 630 635 640
 Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu Glu Tyr
 645 650 655

Asp Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu Ala Asn Trp
 660 665 670
 Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu Leu Gln
 675 680 685
 Lys Asn Met Gln Ile Ala Asn His Thr Leu Lys Tyr Gly Thr Gln Ala
 690 695 700
 Arg Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile Lys Arg Ile
 705 710 715 720
 Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala Gln Glu
 725 730 735
 Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr Tyr Ser
 740 745 750
 Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu Glu Pro
 755 760 765
 Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp Leu Leu
 770 775 780
 Trp Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala Ile Leu Gln
 785 790 795 800
 Phe Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala Arg Leu Asn
 805 810 815
 Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr Glu Thr Pro
 820 825 830
 Ser Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu Gln Pro Leu
 835 840 845
 Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg His Tyr
 850 855 860
 Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala His Leu Leu
 865 870 875 880
 Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu Val Val
 885 890 895
 Pro Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala Met Leu Lys
 900 905 910
 Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp Phe Phe
 915 920 925
 Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys Ser
 930 935 940
 Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser
 945 950 955 960
 Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys Thr
 965 970 975

Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met Gly His
 980 985 990
 Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu Arg Glu
 995 1000 1005
 Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu
 1010 1015 1020
 Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu Ser Ser
 1025 1030 1035 1040
 Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met Lys Met Ala
 1045 1050 1055
 Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val Asp Gln Trp
 1060 1065 1070
 Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn Gln
 1075 1080 1085
 Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro Val
 1090 1095 1100
 Pro Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe His Ile Pro
 1105 1110 1115 1120
 Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile Ile Gln Phe
 1125 1130 1135
 Gln Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr Gly Pro Leu
 1140 1145 1150
 His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln Arg Leu Ala
 1155 1160 1165
 Thr Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu Ala Met Gln
 1170 1175 1180
 Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Leu Ser Tyr
 1185 1190 1195 1200
 Phe Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu Leu His Gly
 1205 1210 1215
 Glu Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn Ser Ala Arg
 1220 1225 1230
 Ser Glu Gly Pro Leu Pro Asp Ser Gly Arg Val Ser Phe Leu Gly Leu
 1235 1240 1245
 Asp Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp Leu Leu Leu Phe
 1250 1255 1260
 Leu Gly Ile Ala Leu Leu Val Ala Thr Leu Gly Leu Ser Gln Arg Leu
 1265 1270 1275 1280
 Phe Ser Ile Arg His Arg Ser Leu His Arg His Ser His Gly Pro Gln
 1285 1290 1295

Phe Gly Ser Glu Val Glu Leu Arg His Ser
 1300 1305

<210> 8
 <211> 1312
 <212> PRT
 <213> Murine sp.

<220>
 <223> Description of Artificial Sequence: motifs

<400> 8
 Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro
 1 5 10 15
 Leu Leu Met Leu Ser Leu Leu Val Leu Leu Leu Gln Pro Ser Pro Ala
 20 25 30
 Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Pro Asp Glu
 35 40 45
 Ala Gly Ala Gln Leu Phe Ala Glu Ser Tyr Asn Ser Ser Ala Glu Val
 50 55 60
 Val Met Phe Gln Ser Thr Val Ala Ser Trp Ala His Asp Thr Asn Ile
 65 70 75 80
 Thr Glu Glu Asn Ala Arg Arg Gln Glu Glu Ala Ala Leu Val Ser Gln
 85 90 95
 Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu Ser
 100 105 110
 Ile Trp Gln Asn Phe Thr Asp Ser Lys Leu Arg Arg Ile Ile Gly Ser
 115 120 125
 Ile Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Gln Arg Gln Gln
 130 135 140
 Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly Lys
 145 150 155 160
 Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Glu
 165 170 175
 Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Lys Leu Leu Phe
 180 185 190
 Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Lys Pro Leu
 195 200 205
 Tyr Gln Asp Phe Thr Ala Ile Ser Asn Glu Ala Tyr Arg Gln Asp Asp
 210 215 220
 Phe Ser Asp Thr Gly Ala Phe Trp Arg Ser Trp Tyr Glu Ser Pro Ser
 225 230 235 240
 Phe Glu Glu Ser Leu Glu His Ile Tyr His Gln Leu Glu Pro Leu Tyr
 245 250 255

Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg Arg Tyr Gly
 260 265 270
 Asp Lys Tyr Val Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly
 275 280 285
 Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro
 290 295 300
 Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys
 305 310 315 320
 Gly Trp Asn Ala Thr His Met Phe Arg Val Ser Glu Glu Phe Phe Thr
 325 330 335
 Ser Leu Gly Leu Ser Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met
 340 345 350
 Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser Ala
 355 360 365
 Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg
 370 375 380
 Val Thr Met Glu Gln Leu Ala Thr Val His His Glu Met Gly His Val
 385 390 395 400
 Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu His Val Ser Leu Arg Arg Gly
 405 410 415
 Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser
 420 425 430
 Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val
 435 440 445
 Thr Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu
 450 455 460
 Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg
 465 470 475 480
 Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp
 485 490 495
 Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Ala
 500 505 510
 Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro Asn
 515 520 525
 Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln
 530 535 540
 Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu His
 545 550 555 560
 Gln Cys Asp Ile Tyr Gln Ser Thr Gln Ala Gly Ala Lys Leu Lys Gln
 565 570 575

Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp
580 585 590

Leu Val Gly Ser Asp Ala Leu Asp Ala Lys Ala Leu Leu Glu Tyr Phe
595 600 605

Gln Pro Val Ser Gln Trp Leu Glu Glu Gln Asn Gln Arg Asn Gly Glu
610 615 620

Val Leu Gly Trp Pro Glu Asn Gln Trp Arg Pro Pro Leu Pro Asp Asn
625 630 635 640

Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asp Arg
645 650 655

Phe Val Glu Glu Tyr Asp Arg Thr Ala Gln Val Leu Leu Asn Glu Tyr
660 665 670

Ala Glu Ala Asn Trp Gln Tyr Asn Thr Asn Ile Thr Ile Glu Gly Ser
675 680 685

Lys Ile Leu Leu Glu Lys Ser Thr Glu Val Ser Asn His Thr Leu Lys
690 695 700

Tyr Gly Thr Arg Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn Ser
705 710 715 720

Ser Ile Lys Arg Ile Ile Lys Lys Leu Gln Asn Leu Asp Arg Ala Val
725 730 735

Leu Pro Pro Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met
740 745 750

Glu Thr Thr Tyr Ser Leu Ser Asn Ile Cys Tyr Thr Asn Gly Thr Cys
755 760 765

Met Pro Leu Glu Pro Asp Leu Thr Asn Met Met Ala Thr Ser Arg Lys
770 775 780

Tyr Glu Glu Leu Leu Trp Ala Trp Lys Ser Trp Arg Asp Lys Val Gly
785 790 795 800

Arg Ala Ile Leu Pro Phe Phe Pro Lys Tyr Val Glu Phe Ser Asn Lys
805 810 815

Ile Ala Lys Leu Asn Gly Tyr Thr Asp Ala Gly Asp Ser Trp Arg Ser
820 825 830

Leu Tyr Glu Ser Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln
835 840 845

Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ser
850 855 860

Leu His Arg His Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro Ile
865 870 875 880

Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile
885 890 895

Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr
 900 905 910
 Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu
 915 920 925
 Ala Asp Asn Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu
 930 935 940
 Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val
 945 950 955 960
 Val Cys His Pro Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg
 965 970 975
 Ile Lys Gln Cys Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His
 980 985 990
 His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro
 995 1000 1005
 Val Thr Phe Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly
 1010 1015 1020
 Asp Ile Met Ala Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu
 1025 1030 1035 1040
 Asn Leu Leu Ser Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe
 1045 1050 1055
 Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr
 1060 1065 1070
 Leu Ile Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys
 1075 1080 1085
 Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly
 1090 1095 1100
 Leu Cys Pro Pro Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser
 1105 1110 1115 1120
 Lys Phe His Val Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser
 1125 1130 1135
 Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly
 1140 1145 1150
 His Thr Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala
 1155 1160 1165
 Gly Lys Leu Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp
 1170 1175 1180
 Pro Glu Ala Met Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser
 1185 1190 1195 1200
 Ala Met Met Asn Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu
 1205 1210 1215

Asn Arg Arg His Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala
 1220 1225 1230

Pro Asn Thr Ala Arg Ala Glu Gly Ser Thr Ala Glu Ser Asn Arg Val
 1235 1240 1245

Asn Phe Leu Gly Leu Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly Gln
 1250 1255 1260

Trp Val Leu Leu Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val Gly
 1265 1270 1275 1280

Leu Ala His Arg Leu Tyr Asn Ile Arg Asn His His Ser Leu Arg Arg
 1285 1290 1295

Pro His Arg Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser
 1300 1305 1310

<210> 9

<211> 1313

<212> PRT

<213> Rattus rattus

<220>

<223> Description of Artificial Sequence: motifs

<400> 9

Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro
 1 5 10 15

Leu Leu Met Leu Ser Leu Leu Leu Leu Leu Leu Pro Pro Ser Pro
 20 25 30

Ala Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Ala Asp
 35 40 45

Glu Ala Gly Ala Gln Leu Phe Ala Asp Ser Tyr Asn Ser Ser Ala Glu
 50 55 60

Val Val Met Phe Gln Ser Thr Ala Ala Ser Trp Ala His Asp Thr Asn
 65 70 75 80

Ile Thr Glu Glu Asn Ala Arg Leu Gln Glu Glu Ala Ala Leu Ile Asn
 85 90 95

Gln Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu
 100 105 110

Ser Ile Trp Gln Asn Phe Thr Asp Gln Lys Leu Arg Arg Ile Ile Gly
 115 120 125

Ser Val Gln Thr Leu Gly Pro Ala Asn Leu Pro Leu Thr Gln Arg Leu
 130 135 140

Gln Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly
 145 150 155 160

Lys Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro
165 170 175

Glu Leu Thr Asn Ile Leu Ala Ser Ser Arg Asn Tyr Ala Lys Val Leu
180 185 190

Phe Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Arg Pro
195 200 205

Leu Tyr Gln Asp Phe Thr Ala Leu Ser Asn Glu Ala Tyr Arg Gln Asp
210 215 220

Gly Phe Ser Asp Thr Gly Ala Tyr Trp Arg Ser Trp Tyr Glu Ser Pro
225 230 235 240

Ser Phe Glu Glu Ser Leu Glu His Leu Tyr His Gln Val Glu Pro Leu
245 250 255

Tyr Leu Asn Leu His Ala Phe Val Arg Arg Ala Leu His Arg Arg Tyr
260 265 270

Gly Asp Lys Tyr Ile Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu
275 280 285

Gly Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val Val
290 295 300

Pro Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln
305 310 315 320

Lys Gly Trp Asn Ala Thr His Met Phe Arg Val Ala Glu Glu Phe Phe
325 330 335

Thr Ser Leu Gly Leu Ser Pro Met Pro Pro Glu Phe Trp Ala Glu Ser
340 345 350

Met Leu Glu Lys Pro Ala Asp Gly Arg Glu Val Val Cys His Ala Ser
355 360 365

Ala Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr
370 375 380

Arg Val Thr Met Asp Gln Leu Ser Thr Val His His Glu Met Gly His
385 390 395 400

Val Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu His Val Ser Leu Arg Arg
405 410 415

Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu
420 425 430

Ser Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp Arg
435 440 445

Val Ala Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala
450 455 460

Leu Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp
465 470 475 480

Arg Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Tyr
 485 490 495
 Asp Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val
 500 505 510
 Ala Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro
 515 520 525
 Ser Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe
 530 535 540
 Gln Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu
 545 550 555 560
 His Gln Cys Asp Ile Tyr Gln Ser Thr Lys Ala Gly Ala Lys Leu Gln
 565 570 575
 Gln Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys
 580 585 590
 Asp Leu Val Gly Ser Asp Ala Leu Asp Ala Ser Ala Leu Met Glu Tyr
 595 600 605
 Phe Gln Pro Val Ser Gln Trp Leu Gln Glu Gln Asn Gln Arg Asn Gly
 610 615 620
 Glu Val Leu Gly Trp Pro Glu Tyr Gln Trp Arg Pro Pro Leu Pro Asp
 625 630 635 640
 Asn Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asn
 645 650 655
 Arg Phe Val Glu Glu Tyr Asp Arg Thr Ala Lys Val Leu Trp Asn Glu
 660 665 670
 Tyr Ala Glu Ala Asn Trp His Tyr Asn Thr Asn Ile Thr Ile Glu Gly
 675 680 685
 Ser Lys Ile Leu Leu Gln Lys Asn Lys Glu Val Ser Asn His Thr Leu
 690 695 700
 Lys Tyr Gly Thr Trp Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn
 705 710 715 720
 Ser Thr Ile Lys Arg Ile Ile Lys Lys Val Gln Asn Val Asp Arg Ala
 725 730 735
 Val Leu Pro Pro Asn Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp
 740 745 750
 Met Glu Thr Thr Tyr Ser Val Ala Asn Val Cys Tyr Thr Asn Gly Thr
 755 760 765
 Cys Leu Ser Leu Glu Pro Asp Leu Thr Asn Ile Met Ala Thr Ser Arg
 770 775 780
 Lys Tyr Glu Glu Leu Leu Trp Val Trp Lys Ser Trp Arg Asp Lys Val
 785 790 795 800

Gly	Arg	Ala	Ile	Leu	Pro	Phe	Phe	Pro	Lys	Tyr	Val	Asp	Phe	Ser	Asn		
				805					810					815			
Lys	Ile	Ala	Lys	Leu	Asn	Gly	Tyr	Ser	Asp	Ala	Gly	Asp	Ser	Trp	Arg		
			820					825					830				
Ser	Ser	Tyr	Glu	Ser	Asp	Asp	Leu	Glu	Gln	Asp	Leu	Glu	Lys	Leu	Tyr		
		835					840					845					
Gln	Glu	Leu	Gln	Pro	Leu	Tyr	Leu	Asn	Leu	His	Ala	Tyr	Val	Arg	Arg		
	850					855					860						
Ser	Leu	His	Arg	His	Tyr	Gly	Ser	Glu	Tyr	Ile	Asn	Leu	Asp	Gly	Pro		
865					870					875					880		
Ile	Pro	Ala	His	Leu	Leu	Gly	Asn	Met	Trp	Ala	Gln	Thr	Trp	Ser	Asn		
				885					890					895			
Ile	Tyr	Asp	Leu	Val	Ala	Pro	Phe	Pro	Ser	Ala	Pro	Ser	Ile	Asp	Ala		
			900					905					910				
Thr	Glu	Ala	Met	Ile	Lys	Gln	Gly	Trp	Thr	Pro	Arg	Arg	Ile	Phe	Lys		
		915					920					925					
Glu	Ala	Asp	Asn	Phe	Phe	Thr	Ser	Leu	Gly	Leu	Leu	Pro	Val	Pro	Pro		
	930					935					940						
Glu	Phe	Trp	Asn	Lys	Ser	Met	Leu	Glu	Lys	Pro	Thr	Asp	Gly	Arg	Glu		
945					950					955					960		
Val	Val	Cys	His	Ala	Ser	Ala	Trp	Asp	Phe	Tyr	Asn	Gly	Lys	Asp	Phe		
				965					970					975			
Arg	Ile	Lys	Gln	Cys	Thr	Ser	Val	Asn	Met	Glu	Glu	Leu	Val	Ile	Ala		
			980					985					990				
His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Phe	Met	Gln	Tyr	Lys	Asp	Leu		
		995					1000					1005					
Pro	Val	Thr	Phe	Arg	Glu	Gly	Ala	Asn	Pro	Gly	Phe	His	Glu	Ala	Ile		
	1010					1015					1020						
Gly	Asp	Val	Leu	Ala	Leu	Ser	Val	Ser	Thr	Pro	Lys	His	Leu	His	Ser		
1025					1030					1035				1040			
Leu	Asn	Leu	Leu	Ser	Ser	Glu	Gly	Ser	Gly	Tyr	Glu	His	Asp	Ile	Asn		
			1045					1050					1055				
Phe	Leu	Met	Lys	Met	Ala	Leu	Asp	Lys	Ile	Ala	Phe	Ile	Pro	Phe	Ser		
		1060						1065				1070					
Tyr	Leu	Ile	Asp	Gln	Trp	Arg	Trp	Arg	Val	Phe	Asp	Gly	Ser	Ile	Thr		
	1075					1080						1085					
Lys	Glu	Asn	Tyr	Asn	Gln	Glu	Trp	Trp	Ser	Leu	Arg	Leu	Lys	Tyr	Gln		
	1090					1095					1100						
Gly	Leu	Cys	Pro	Pro	Val	Pro	Arg	Ser	Gln	Gly	Asp	Phe	Asp	Pro	Gly		
1105					1110					1115				1120			

Ser	Lys	Phe	His	Val	Pro	Ala	Asn	Val	Pro	Tyr	Ile	Arg	Tyr	Phe	Ile	
				1125						1130					1135	
Ser	Phe	Ile	Ile	Gln	Phe	Gln	Phe	His	Glu	Ala	Leu	Cys	Arg	Ala	Ala	
			1140					1145					1150			
Gly	His	Thr	Gly	Pro	Leu	Tyr	Lys	Cys	Asp	Ile	Tyr	Gln	Ser	Lys	Glu	
		1155					1160					1165				
Ala	Gly	Lys	Leu	Leu	Ala	Asp	Ala	Met	Lys	Leu	Gly	Tyr	Ser	Lys	Gln	
	1170					1175					1180					
Trp	Pro	Glu	Ala	Met	Lys	Ile	Ile	Thr	Gly	Gln	Pro	Asn	Met	Ser	Ala	
1185					1190					1195					1200	
Ser	Ala	Ile	Met	Asn	Tyr	Phe	Lys	Pro	Leu	Thr	Glu	Trp	Leu	Val	Thr	
			1205						1210					1215		
Glu	Asn	Arg	Arg	His	Gly	Glu	Thr	Leu	Gly	Trp	Pro	Glu	Tyr	Thr	Trp	
		1220						1225					1230			
Thr	Pro	Asn	Thr	Ala	Arg	Ala	Glu	Gly	Ser	Leu	Pro	Glu	Ser	Ser	Arg	
	1235						1240					1245				
Val	Asn	Phe	Leu	Gly	Met	Tyr	Leu	Glu	Pro	Gln	Gln	Ala	Arg	Val	Gly	
	1250				1255						1260					
Gln	Trp	Val	Leu	Leu	Phe	Leu	Gly	Val	Ala	Leu	Leu	Val	Ala	Thr	Val	
1265				1270						1275					1280	
Gly	Leu	Ala	His	Arg	Leu	Tyr	Asn	Ile	His	Asn	His	His	Ser	Leu	Arg	
			1285					1290						1295		
Arg	Pro	His	Arg	Gly	Pro	Gln	Phe	Gly	Ser	Glu	Val	Glu	Leu	Arg	His	
		1300						1305					1310			

Ser

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<210> 10
<211> 1310
<212> PRT
<213> Oryctolagus cuniculus
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<220>
<223> Description of Artificial Sequence: motifs
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<400> 10
Met Gly Ala Ala Pro Gly Arg Arg Gly Pro Arg Leu Leu Arg Pro Pro
1 5 10 15
Pro Pro Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Pro Ala Ala
20 25 30
Leu Thr Leu Asp Pro Gly Leu Leu Pro Gly Asp Phe Ala Ala Asp Glu
35 40 45
Ala Gly Ala Arg Leu Phe Ala Ser Ser Tyr Asn Ser Ser Ala Glu Gln
50 55 60

Val Leu Phe Arg Ser Thr Ala Ala Ser Trp Ala His Asp Thr Asn Ile
 65 70 75 80
 Thr Ala Glu Asn Ala Arg Arg Gln Glu Glu Glu Ala Leu Leu Ser Gln
 85 90 95
 Glu Phe Ala Glu Ala Trp Gly Lys Lys Ala Lys Glu Leu Tyr Asp Pro
 100 105 110
 Val Trp Gln Asn Phe Thr Asp Pro Glu Leu Arg Arg Ile Ile Gly Ala
 115 120 125
 Val Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln
 130 135 140
 Tyr Asn Ser Leu Leu Ser Asn Met Ser Gln Ile Tyr Ser Thr Gly Lys
 145 150 155 160
 Val Cys Phe Pro Asn Lys Thr Ala Ser Cys Trp Ser Leu Asp Pro Asp
 165 170 175
 Leu Asn Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe
 180 185 190
 Ala Trp Glu Gly Trp His Asn Ala Val Gly Ile Pro Leu Lys Pro Leu
 195 200 205
 Tyr Gln Glu Phe Thr Ala Leu Ser Asn Glu Ala Tyr Arg Gln Asp Gly
 210 215 220
 Phe Ser Asp Thr Gly Ala Tyr Trp Arg Ser Trp Tyr Asp Ser Pro Thr
 225 230 235 240
 Phe Glu Glu Asp Leu Glu Arg Ile Tyr His Gln Leu Glu Pro Leu Tyr
 245 250 255
 Leu Asn Leu His Ala Tyr Val Arg Arg Val Leu His Arg Arg Tyr Gly
 260 265 270
 Asp Arg Tyr Ile Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly
 275 280 285
 Asn Met Trp Ala Gln Ser Trp Glu Ser Ile Tyr Asp Met Val Val Pro
 290 295 300
 Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys
 305 310 315 320
 Gly Trp Asn Ala Thr His Met Phe Arg Val Ala Glu Glu Phe Phe Thr
 325 330 335
 Ser Leu Gly Leu Leu Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met
 340 345 350
 Leu Glu Lys Pro Glu Asp Gly Arg Glu Val Val Cys His Ala Ser Ala
 355 360 365
 Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Gln
 370 375 380

Val Thr Met Asp Gln Leu Ser Thr Val His His Glu Met Gly His Val
 385 390 395 400
 Gln Tyr Tyr Leu Gln Tyr Lys Asp Gln Pro Val Ser Leu Arg Arg Ala
 405 410 415
 Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val
 420 425 430
 Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val Thr
 435 440 445
 Asn Asp Thr Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu
 450 455 460
 Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp
 465 470 475 480
 Gly Val Phe Ser Gly Arg Thr Pro Ser Ser Arg Tyr Asn Phe Asp Trp
 485 490 495
 Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Val Arg
 500 505 510
 Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro Ser Val
 515 520 525
 Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe
 530 535 540
 His Gln Ala Leu Cys Met Glu Ala Gly His Gln Gly Pro Leu His Gln
 545 550 555 560
 Cys Asp Ile Tyr Gln Ser Thr Arg Ala Gly Ala Lys Leu Arg Ala Val
 565 570 575
 Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met
 580 585 590
 Val Ala Ser Asp Ala Leu Asp Ala Gln Pro Leu Leu Asp Tyr Phe Gln
 595 600 605
 Pro Val Thr Gln Trp Leu Gln Glu Gln Asn Glu Arg Asn Gly Glu Val
 610 615 620
 Leu Gly Trp Pro Glu Tyr Gln Trp Arg Pro Pro Leu Pro Asn Asn Tyr
 625 630 635 640
 Pro Glu Gly Ile Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Arg Phe
 645 650 655
 Val Glu Glu Tyr Asp Arg Ser Phe Gln Ala Val Trp Asn Glu Tyr Ala
 660 665 670
 Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu Ala Ser Lys
 675 680 685
 Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr Leu Thr Tyr
 690 695 700

Gly Asn Trp Ala Arg Arg Phe Asp Val Ser Asn Phe Gln Asn Ala Thr
 705 710 715 720
 Ser Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Gln Arg Ala Val Leu
 725 730 735
 Pro Val Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met Glu
 740 745 750
 Thr Ile Tyr Ser Val Ala Asn Val Cys Arg Val Asp Gly Ser Cys Leu
 755 760 765
 Gln Leu Glu Pro Asp Leu Thr Asn Leu Met Ala Thr Ser Arg Lys Tyr
 770 775 780
 Asp Glu Leu Leu Trp Val Trp Thr Ser Trp Arg Asp Lys Val Gly Arg
 785 790 795 800
 Ala Ile Leu Pro Tyr Phe Pro Lys Tyr Val Glu Phe Thr Asn Lys Ala
 805 810 815
 Ala Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met
 820 825 830
 Tyr Glu Thr Pro Thr Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu
 835 840 845
 Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Gly Arg Ala Leu
 850 855 860
 His Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro
 865 870 875 880
 Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr
 885 890 895
 Asp Leu Val Ala Pro Phe Pro Ser Ala Ser Thr Met Asp Ala Thr Glu
 900 905 910
 Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Met Phe Glu Glu Ala
 915 920 925
 Asp Lys Phe Phe Ile Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe
 930 935 940
 Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val
 945 950 955 960
 Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile
 965 970 975
 Lys Gln Cys Thr Thr Val Asn Met Glu Asp Leu Val Val Val His His
 980 985 990
 Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val
 995 1000 1005
 Ala Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp
 1010 1015 1020

Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser Ile Asn
 1025 1030 1035 1040
 Leu Leu Ser Ser Glu Gly Gly Gly Tyr Glu His Asp Ile Asn Phe Leu
 1045 1050 1055
 Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu
 1060 1065 1070
 Val Asp Glu Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu
 1075 1080 1085
 Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu
 1090 1095 1100
 Cys Pro Pro Ala Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ala Lys
 1105 1110 1115 1120
 Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe
 1125 1130 1135
 Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Lys Ala Ala Gly His
 1140 1145 1150
 Thr Gly Pro Leu His Thr Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly
 1155 1160 1165
 Lys Arg Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp Pro
 1170 1175 1180
 Glu Ala Met Lys Val Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala
 1185 1190 1195 1200
 Met Met Asn Tyr Phe Lys Pro Leu Met Asp Trp Leu Leu Thr Glu Asn
 1205 1210 1215
 Gly Arg His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Thr Trp Thr Pro
 1220 1225 1230
 Asn Ser Ala Arg Ser Glu Gly Ser Leu Pro Asp Ser Gly Arg Val Asn
 1235 1240 1245
 Phe Leu Gly Met Asn Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp
 1250 1255 1260
 Val Leu Leu Phe Leu Gly Val Ala Leu Leu Leu Ala Ser Leu Gly Leu
 1265 1270 1275 1280
 Thr Gln Arg Leu Phe Ser Ile Arg Tyr Gln Ser Leu Arg Gln Pro His
 1285 1290 1295
 His Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser
 1300 1305 1310

<210> 11
 <211> 615
 <212> PRT
 <213> *Drosophila melanogaster*
 <220>

<223> Description of Artificial Sequence: motifs

<400> 11

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Met Arg Leu Phe Leu Leu Ala Leu Leu Ala Thr Leu Ala Val Thr Gln
 1           5           10           15

Ala Leu Val Lys Glu Glu Ile Gln Ala Lys Glu Tyr Leu Glu Asn Leu
 20           25           30

Asn Lys Glu Leu Ala Lys Arg Thr Asn Val Glu Thr Glu Ala Ala Trp
 35           40           45

Ala Tyr Gly Ser Asn Ile Thr Asp Glu Asn Glu Lys Lys Lys Asn Glu
 50           55           60

Ile Ser Ala Glu Leu Ala Lys Phe Met Lys Glu Val Ala Ser Asp Thr
 65           70           75           80

Thr Lys Phe Gln Trp Arg Ser Tyr Gln Ser Glu Asp Leu Lys Arg Gln
 85           90           95

Phe Lys Ala Leu Thr Lys Leu Gly Tyr Ala Ala Leu Pro Glu Asp Asp
100           105           110

Tyr Ala Glu Leu Leu Asp Thr Leu Ser Ala Met Glu Ser Asn Phe Ala
115           120           125

Lys Val Lys Val Cys Asp Tyr Lys Asp Ser Thr Lys Cys Asp Leu Ala
130           135           140

Leu Asp Pro Glu Ile Glu Glu Val Ile Ser Lys Ser Arg Asp His Glu
145           150           155           160

Glu Leu Ala Tyr Tyr Trp Arg Glu Phe Tyr Asp Lys Ala Gly Thr Ala
165           170           175

Val Arg Ser Gln Phe Glu Arg Tyr Val Glu Leu Asn Thr Lys Ala Ala
180           185           190

Lys Leu Asn Asn Phe Thr Ser Gly Ala Glu Ala Trp Leu Asp Glu Tyr
195           200           205

Glu Asp Asp Thr Phe Glu Gln Gln Leu Glu Asp Ile Phe Ala Asp Ile
210           215           220

Arg Pro Leu Tyr Gln Gln Ile His Gly Tyr Val Arg Phe Arg Leu Arg
225           230           235           240

Lys His Tyr Gly Asp Ala Val Val Ser Glu Thr Gly Pro Ile Pro Met
245           250           255

His Leu Leu Gly Asn Met Trp Ala Gln Gln Trp Ser Glu Ile Ala Asp
260           265           270

Ile Val Ser Pro Phe Pro Glu Lys Pro Leu Val Asp Val Ser Ala Glu
275           280           285

Met Glu Lys Gln Ala Tyr Thr Pro Leu Lys Met Phe Gln Met Gly Asp
290           295           300

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<210> 12
<211> 907
<212> PRT
<213> Caenorhabditis elegans

<220>

<223> Description of Artificial Sequence: motifs

<400> 12

Met	Lys	Phe	His	Ile	Leu	Leu	Leu	Leu	Leu	Val	Gly	Ala	Cys	Leu	Pro
1				5					10					15	
Val	Phe	Thr	Gln	Glu	Ile	Lys	Pro	Lys	Pro	Glu	Leu	Leu	Pro	Ala	Asp
			20					25					30		
Glu	Ala	Pro	Lys	Asp	Pro	Glu	Ala	Val	Phe	Ser	Glu	Gly	Glu	Pro	Phe
		35					40					45			
Glu	Leu	Thr	Asp	Ala	Leu	Asp	Thr	Pro	Lys	Asn	Gly	Ser	Val	Pro	Val
	50					55					60				
Pro	Glu	Pro	Glu	Pro	Lys	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Lys
65					70				75						80
Pro	Glu	Pro	Glu	Pro	Ser	Pro	Thr	Pro	Glu	Pro	Glu	Pro	Ala	Ile	Lys
				85					90					95	
Phe	Asp	Asn	Ile	Glu	Ser	Glu	Asp	Tyr	Gly	Asp	Val	Ala	Glu	Thr	Ala
			100					105					110		
Ala	Ser	Thr	Gln	Pro	Asp	Glu	Leu	Asn	Thr	Glu	Val	Ile	Glu	Gln	Leu
		115					120					125			
Val	Asp	Thr	Phe	Leu	Asn	Thr	Gly	Ser	Ile	Ala	Ser	Asn	Lys	Thr	Asn
	130					135					140				
Lys	Gly	Pro	Val	Phe	Ala	Asn	Pro	Val	Ala	Gln	Ala	Leu	Val	Asn	Ser
145					150					155				160	
Ser	Asn	Tyr	Trp	Lys	Thr	Asp	Asn	Leu	Gln	Ala	Pro	Gly	Ser	Ile	Lys
				165				170						175	
Asp	Glu	Glu	Lys	Leu	Arg	Ser	Trp	Leu	Ala	Gly	Tyr	Glu	Ala	Glu	Ala
			180					185					190		
Ile	Lys	Val	Leu	Arg	Glu	Val	Ala	Leu	Ser	Gly	Trp	Arg	Tyr	Phe	Asn
		195					200					205			
Asp	Ala	Ser	Pro	Ser	Leu	Lys	Leu	Ala	Leu	Asp	Glu	Ala	Glu	Asn	Val
	210					215					220				
Leu	Thr	Met	Phe	Val	Arg	Ser	Thr	Ser	Met	Gln	Ala	Lys	Gln	Phe	Asp
225					230					235					240
Met	Ala	Ser	Val	Thr	Asp	Glu	Lys	Val	Met	Arg	Gln	Leu	Gly	Tyr	Val
				245					250					255	
Ser	Phe	Glu	Gly	Met	Ser	Ala	Leu	Ala	Pro	Ser	Arg	Phe	Ala	Asp	Tyr
			260				265						270		

Ser Gln Ala Gln Ala Ala Leu Asn Arg Asp Ser Lys Asp Ser Thr Ile
 275 280 285
 Cys Asp Lys Asp Val Pro Pro Pro Cys Ala Leu Gln Lys Ile Asp Met
 290 295 300
 Asp Ser Ile Phe Arg Asn Glu Lys Asp Ala Ser Arg Leu Gln His Leu
 305 310 315 320
 Trp Val Ser Tyr Val Thr Ala Ile Ala Lys Ser Lys Pro Ser Tyr Asn
 325 330 335
 Asn Ile Ile Thr Ile Ser Asn Glu Gly Ala Lys Leu Asn Gly Phe Ala
 340 345 350
 Asn Gly Gly Ala Met Trp Arg Ser Ala Phe Asp Met Ser Ser Lys Val
 355 360 365
 His Lys Ala Glu Phe Asp Leu Asn Lys Gln Ile Asp Lys Ile Tyr Ser
 370 375 380
 Thr Ile Gln Pro Phe Tyr Gln Leu Leu His Ala Tyr Met Arg Arg Gln
 385 390 395 400
 Leu Ala Gly Ile Tyr Ser Asn Pro Val Gly Leu Ser Lys Asp Gly Pro
 405 410 415
 Ile Pro Ala His Leu Phe Gly Ser Leu Asp Gly Gly Asp Trp Ser Ala
 420 425 430
 His Tyr Glu Gln Thr Lys Pro Phe Glu Glu Glu Ser Glu Thr Pro Glu
 435 440 445
 Ala Met Leu Ser Ala Phe Asn Thr Gln Asn Tyr Thr Thr Lys Lys Met
 450 455 460
 Phe Val Thr Ala Tyr Arg Tyr Phe Lys Ser Ala Gly Phe Pro His Leu
 465 470 475 480
 Pro Lys Ser Tyr Trp Thr Ser Ser Ile Phe Ala Arg Val Trp Ser Lys
 485 490 495
 Asp Met Ile Cys His Pro Ala Ala Ala Leu Asp Met Arg Ala Pro Asn
 500 505 510
 Asp Phe Arg Val Lys Ala Cys Ala Gln Leu Gly Glu Pro Asp Phe Glu
 515 520 525
 Gln Ala His Ser Leu Leu Val Gln Thr Tyr Tyr Gln Tyr Leu Tyr Lys
 530 535 540
 Asp Gln Ser Leu Leu Phe Arg Glu Gln Ala Ser Pro Val Ile Thr Asp
 545 550 555 560
 Ala Ile Ala Asn Ala Phe Ala His Leu Ser Thr Asn Pro His Tyr Leu
 565 570 575
 Tyr Ser Gln Lys Leu Val Pro Ser Glu His Leu Asp Ile Lys Asp Ser
 580 585 590

Val Ile Ile Asn Lys Leu Tyr Lys Glu Ser Leu Glu Ser Phe Thr Lys
 595 600 605
 Leu Pro Phe Thr Ile Ala Ala Asp Asn Trp Arg Tyr Glu Leu Phe Asp
 610 615 620
 Gly Thr Val Pro Lys Asn Lys Leu Asn Asp Arg Trp Trp Glu Ile Arg
 625 630 635 640
 Asn Lys Tyr Glu Gly Val Arg Ser Pro Gln Pro Tyr Asn Thr Ser Asn
 645 650 655
 Leu Asp Ala Leu Ile His Asn Ser Val Ser Gln Val His Ser Pro Ala
 660 665 670
 Thr Arg Thr Leu Ile Ser Tyr Val Leu Lys Phe Gln Ile Leu Lys Ala
 675 680 685
 Leu Cys Gln Arg Glu Leu Phe Trp Leu Ser Glu Gly Cys Ile Leu Ser
 690 695 700
 Glu Asp Thr Thr Glu Lys Leu Arg Glu Thr Met Lys Leu Gly Ser Ser
 705 710 715 720
 Ile Thr Trp Leu Lys Ala Leu Glu Met Ile Ser Gly Lys Gly Glu Leu
 725 730 735
 Asp Ala Gln Pro Leu Leu Glu Tyr Tyr Glu Pro Leu Ile Asn Trp Leu
 740 745 750
 Arg Asn Thr Asn Glu Ile Asp Gln Val Val Val Gly Trp Asp Gly Glu
 755 760 765
 Gly Thr Pro Phe Thr Val Glu Glu Ile Pro Lys Thr Arg Gln Pro Gly
 770 775 780
 Asp Gly Gly Asn Gly Leu Pro Ser Glu Asp Arg Val Ala Phe Pro Gly
 785 790 795 800
 Gly Glu Cys Val Asn Gly Gln Glu Cys Leu Leu Asp Ser His Cys Asn
 805 810 815
 Gly Thr Ile Cys Val Cys Asn Asp Gly Leu Tyr Thr Leu Glu Ile Gly
 820 825 830
 Asn Thr Phe Asn Cys Val Pro Gly Asn Pro Ala Asp Ser Gly Phe Gly
 835 840 845
 Asp Gly Lys Gly Gly Leu Val Ile Gly Leu Phe Asn Asn Glu Val Thr
 850 855 860
 Thr Pro Glu Pro Ser Ala Glu Pro Glu Pro Thr Ala Lys Thr Thr Thr
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 Lys Met Pro Pro Arg Val Arg Ala Ala Thr Ser Pro Phe Ser Leu Tyr
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